Claims

1. A method of identifying a base at a target position in a sample nucleic acid sequence wherein a primer, which hybridises to the sample nucleic acid immediately adjacent to the target position, is provided and the sample nucleic acid and primer are subjected to a polymerase reaction in the presence of a nucleotide whereby the nucleotide will only become incorporated if it is complementary to the base in the target position, and said incorporation is detected, characterised in that, a single-stranded nucleic acid binding protein is included in the polymerase reaction step.

2. A method as claimed in claim 1 wherein the single-stranded nucleic acid binding protein is selected from the group comprising *E. coli* single-stranded binding protein (Eco SSB), T4 gene 32 protein (T4 gp32), T7 SSB, coliphage N4 SSB, T4 gene 44/62 protein, adenovirus DNA binding protein (AdDBP or AdSSB) and calf thymus unwinding protein (UP1).

3. A method as claimed in claim 2 wherein the single-stranded nucleic acid binding protein is Eco SSB.

4. A method as claimed in any of the preceding claims wherein the sample nucleic acid is DNA.

5. A method as claimed in any of the preceding claims wherein the single-stranded nucleic acid binding protein binds to the sample nucleic acid.

6. A method as claimed in any of the preceding claims wherein the incorporation of the nucleotide is detected by monitoring the release of inorganic pyrophosphate.

7. A method as claimed in claim 6 wherein the release of inorganic pyrophosphate is detected using ATP sulphurylase and luciferase.

8. A method as claimed in any of the preceding claims wherein apyrase is present during the polymerase reaction.

9. A method as claimed in any one of the preceding claims wherein the single-stranded nucleic acid binding protein is added after hybridisation of the primer to the sample nucleic acid.

10. A method as claimed in any one of the preceding claims wherein at least 25 bases in the nucleic acid sample are identified.

11. Use of a single-stranded nucleic acid binding protein in a nucleic acid sequencing-by-synthesis method.

12. A method of enhancing the activity of a nucleotide-degrading enzyme when used in a nucleic acid sequencing-by-synthesis method, which comprises the use of a single-stranded nucleic acid binding protein.

13. A method of enhancing the activity of luciferase when used as a detection enzyme in a nucleic acid sequencing-by-synthesis method which comprises the use of a single-stranded nucleic acid binding protein.

14. A method of maintaining a constant signal intensity during a method of nucleic acid sequencing-by-synthesis comprising the use of a single-stranded nucleic acid binding protein.

15. A kit for use in a method of sequencing-by-synthesis which comprises nucleotides for incorporation, a polymerase, means for detection of incorporation and a single-stranded nucleic acid binding protein.